

SEQUENCE LISTING

<110> Givaudan SA

<120> G-Proteins

<130> 30069PCT

<150> US 60/434,790

<151> 2002-12-18

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<170> PatentIn version 3.1

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<212> DNA

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ttg gag cag aag aag cag gac cgc ggg gag ctg aag ctg ctg ctt ttg 144

35 40 45

ggc cca ggc gag agc ggg aag agc acc ttc atc aag cag atg cgg atc 192

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atc cac ggc gcc ggc tac tcg gag gag gag cgc aag ggc ttc cg^g ccc 240
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ctg gtc tac cag aac atc ttc gt^g tcc at^g cg^g gcc at^g atc gag gcc 288
85 90 95

at^g gag cg^g ctg cag att cca ttc agc agg ccc gag agc aag cac cac 336
100 105 110

gct agc ctg gtc at^g agc cag gac ccc tat aaa gt^g acc acg ttt gag 384
115 120 125

aag cg^c tac gct gcg gcc at^g cag tgg ctg tgg agg gat gcc ggc atc 432
130 135 140

cg^g gcc tgc tat gag cgt cg^g cg^g gaa ttc cac ctg ctc gat tca gcc 480
145 150 155 160

gt^g tac tac ctg tcc cac ctg gag cg^c atc acc gag gag gg^c tac gtc 528
165 170 175

ccc aca gct cag gag gt^g ctc cg^c agc cg^c at^g ccc acc act gg^c atc 576
180 185 190

aac gag tac tgc ttc tcc gt^g cag aaa acc aac ctg cg^g atc gt^g gag 624
195 200 205

gt^c ggg ggc cag aag tca gag cgt aag aaa tgg atc cat tgt ttc gag 672
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aac gtg atc gcc ctc atc tac ctg gcc tca ctg agt gaa tac gac cag 720
225 230 235 240

tgc ctg gag gag aac aac cag gag aac cgc atg aag gag agc ctc gca 768
245 250 255

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260 265 270

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275 280 285

tcc cac ctg gct acc tat ttc ccc agt ttc cag ggc cct aag cag gat 912
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gct gag gca gcc aag agg ttc atc ctg gac atg tac acg agg atg tac 960
305 310 315 320

acc ggg tgc gtg gac ggc ccc gag ggc agc aac tta aaa aaa gaa gat 1008
325 330 335

aag gaa atc tat tct cac atg acc tgc gct act gac aca caa aac gtc 1056
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aaa gac tgt ggg ctc ttc 1122
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35 40 45

Gly Pro Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg Ile

50 55 60

Ile His Gly Ala Gly Tyr Ser Glu Glu Glu Arg Lys Gly Phe Arg Pro

65 70 75 80

Leu Val Tyr Gln Asn Ile Phe Val Ser Met Arg Ala Met Ile Glu Ala

85 90 95

Met Glu Arg Leu Gln Ile Pro Phe Ser Arg Pro Glu Ser Lys His His

100 105 110

Ala Ser Leu Val Met Ser Gln Asp Pro Tyr Lys Val Thr Thr Phe Glu

115 120 125

Lys Arg Tyr Ala Ala Ala Met Gln Trp Leu Trp Arg Asp Ala Gly Ile

130 135 140

Arg Ala Cys Tyr Glu Arg Arg Arg Glu Phe His Leu Leu Asp Ser Ala

145 150 155 160

Val Tyr Tyr Leu Ser His Leu Glu Arg Ile Thr Glu Glu Gly Tyr Val

165 170 175

Pro Thr Ala Gln Asp Val Leu Arg Ser Arg Met Pro Thr Thr Gly Ile

180 185 190

Asn Glu Tyr Cys Phe Ser Val Gln Lys Thr Asn Leu Arg Ile Val Asp

195 200 205

Val Gly Gly Gln Lys Ser Glu Arg Lys Lys Trp Ile His Cys Phe Glu

210 215 220

Asn Val Ile Ala Leu Ile Tyr Leu Ala Ser Leu Ser Glu Tyr Asp Gln

225 230 235 240

Cys Leu Glu Glu Asn Asn Gln Glu Asn Arg Met Lys Glu Ser Leu Ala

245 250 255

Leu Phe Gly Thr Ile Leu Glu Leu Pro Trp Phe Lys Ser Thr Ser Val

260 265 270

Ile Leu Phe Leu Asn Lys Thr Asp Ile Leu Glu Glu Lys Ile Pro Thr

275 280 285

Ser His Leu Ala Thr Tyr Phe Pro Ser Phe Gln Gly Pro Lys Gln Asp

290 295 300

Ala Glu Ala Ala Lys Arg Phe Ile Leu Asp Met Tyr Thr Arg Met Tyr

305 310 315 320

Thr Gly Cys Val Asp Gly Pro Glu Gly Ser Asn Leu Lys Lys Glu Asp

325 330 335

Lys Glu Ile Tyr Ser His Met Thr Cys Ala Thr Asp Thr Gln Asn Val

340 345 350

Lys Phe Val Phe Asp Ala Val Thr Asp Ile Ile Ile Lys Glu Asn Leu

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Lys Asp Cys Gly Leu Phe

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